```
     (FILE 'HOME' ENTERED AT 11:31:21 ON 25 SEP 2000)

     INDEX 'ADISALERTS, ADISINSIGHT, AGRICOLA, AIDSLINE, ANABSTR, AQUASCI,
     BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO,
CABA,
     CANCERLIT, CAPLUS, CEABA, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU,
     DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, ...' ENTERED AT 11:31:31 ON 25 SEP
     2000
               SEA CARTILAGE OLIGOMERIC MATRIX PROTEIN
               ---------
              10   FILE ADISALERTS
               1   FILE AGRICOLA
               1   FILE BIOCOMMERCE
             149   FILE BIOSIS
               2   FILE BIOTECHABS
               2   FILE BIOTECHDS
              69   FILE BIOTECHNO
               6   FILE CABA
              14   FILE CANCERLIT
             101   FILE CAPLUS
               3   FILE CONFSCI
               4   FILE DDFU
              47   FILE DGENE
               4   FILE DRUGU
               7   FILE EMBAL
             112   FILE EMBASE
              73   FILE ESBIOBASE
              28   FILE GENBANK
               3   FILE JICST-EPLUS
              36   FILE LIFESCI
             114   FILE MEDLINE
               2   FILE PROMT
             141   FILE SCISEARCH
               6   FILE TOXLINE
              13   FILE TOXLIT
               4   FILE USPATFULL
               8   FILE WPIDS
               8   FILE WPINDEX
L1             QUE CARTILAGE OLIGOMERIC MATRIX PROTEIN
               ---------
               SEA L1 AND (VARIANT? OR SPLICE)
               ---------
               6   FILE BIOSIS
               5   FILE BIOTECHNO
               4   FILE CAPLUS
               2   FILE EMBAL
               6   FILE EMBASE
               4   FILE ESBIOBASE
               2   FILE LIFESCI
               5   FILE MEDLINE
               5   FILE SCISEARCH
               3   FILE USPATFULL
L2             QUE L1 AND (VARIANT? OR SPLICE)
               ---------

     FILE 'BIOSIS, EMBASE, BIOTECHNO, MEDLINE, SCISEARCH, CAPLUS, ESBIOBASE,
     USPATFULL, EMBAL, LIFESCI' ENTERED AT 11:38:50 ON 25 SEP 2000
L3          42 S L1 AND (VARIANT? OR SPLICE)
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                1*  FILE FSTA
                0*  FILE KOSMET
                0*  FILE MEDICONF
                3   FILE MEDLINE
                0*  FILE NTIS
                1   FILE SCISEARCH
                2   FILE TOXLINE
               10   FILE USPATFULL
L2               QUE L1 AND (DIET OR EAT? OR INGEST?)
                 ---------

     FILE 'USPATFULL, BIOSIS, CABA, CAPLUS, EMBASE, MEDLINE, TOXLINE,
     AGRICOLA, DRUGU, SCISEARCH, FSTA' ENTERED AT 07:02:03 ON 25 SEP 2000
L3          3315 S SOY(15W)(DIET OR EAT? OR INGEST?)
L4           193 S L3 AND (DIET OR EAT? OR INGEST?)(15W)LIVER
L5             2 S L4 AND LIVER(15W)(ENLARG? OR SWELL?)
L6             3 S L4 AND TRYPSIN
L7             3 DUP REM L6 (0 DUPLICATES REMOVED)
L8             5 S L3 AND SOY(15W)(ENLARG?)
L9             2 DUP REM L8 (3 DUPLICATES REMOVED)

     INDEX 'ADISALERTS, ADISINSIGHT, AGRICOLA, AIDSLINE, ANABSTR, AQUASCI,
     BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO,
CABA,
     CANCERLIT, CAPLUS, CEABA, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU,
     DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, ...' ENTERED AT 07:12:39 ON 25 SEP
     2000
                 SEA (PROTEIN? OR PEPTIDE?)(15W)(AGGREGAT? OR OLIGOMERIZ?)
                 ---------
                45   FILE ADISALERTS
                15   FILE ADISINSIGHT
               429   FILE AGRICOLA
               101   FILE AIDSLINE
                41   FILE ANABSTR
               133   FILE AQUASCI
               354   FILE BIOBUSINESS
                36   FILE BIOCOMMERCE
              8129   FILE BIOSIS
               460   FILE BIOTECHABS
               460   FILE BIOTECHDS
              3317   FILE BIOTECHNO
               907   FILE CABA
               912   FILE CANCERLIT
              9886   FILE CAPLUS
               152   FILE CEABA
                55   FILE CEN
                33   FILE CIN
                77   FILE CONFSCI
                 5   FILE CROPB
                10   FILE CROPU
               178   FILE DDFB
               309   FILE DDFU
              2645   FILE DGENE
               178   FILE DRUGB
                 5   FILE DRUGNL
               540   FILE DRUGU
                83   FILE EMBAL
              6750   FILE EMBASE
              2554   FILE ESBIOBASE
               417   FILE FROSTI
               777   FILE FSTA
                31   FILE GENBANK
                 4   FILE HEALSAFE
               318   FILE IFIPAT
               366   FILE JICST-EPLUS
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              12   FILE KOSMET
            2360   FILE LIFESCI
               2   FILE MEDICONF
            6438   FILE MEDLINE
              37   FILE NIOSHTIC
              72   FILE NTIS
              25   FILE OCEAN
              10   FILE PHAR
              30   FILE PHIN
             173   FILE PROMT
            5489   FILE SCISEARCH
            1071   FILE TOXLINE
            1590   FILE TOXLIT
            3132   FILE USPATFULL
             552   FILE WPIDS
             552   FILE WPINDEX
L10             QUE (PROTEIN? OR PEPTIDE?)(15W)(AGGREGAT? OR OLIGOMERIZ?)
                ---------

     FILE 'CAPLUS, BIOSIS, EMBASE, MEDLINE, SCISEARCH, BIOTECHNO, USPATFULL,
     DGENE, ESBIOBASE, LIFESCI, TOXLIT, TOXLINE, CANCERLIT, CABA, FSTA,
WPIDS,
     DRUGU, BIOTECHDS, AGRICOLA, FROSTI, JICST-EPLUS, BIOBUSINESS, IFIPAT,
     DRUGB, PROMT, CEABA, AQUASCI, AIDSLINE, ...' ENTERED AT 07:16:39 ON 25
     SEP 2000
L11          4850 S (PROTEIN? OR PEPTIDE?)(15W)(OLIGOMERIZ?)
L12           117 S L11 AND PENTA?
L13            61 DUP REM L12 (56 DUPLICATES REMOVED)
L14            35 S L12 AND SPACE?
L15            28 DUP REM L14 (7 DUPLICATES REMOVED)
L16            14 S L15 AND PROLINE
```

cytotoxin at pH 7.4 measured by CD- and ATR-FTIR-spectroscopy consists of about 50 % .beta.-sheet, 10 % .alpha.-helix as well as 40 % .beta.-turn and random coil. Decreasing medium pH to 6.0 does not notably influence the FTIR spectrum. But incubation with SDS results in a rise to about 70 % .beta.-structure, consisting of long, antiparallel .beta.-sheets. The detergent OPOE increases the amt. of .beta.-structure to approx. 55-60 %. The spectrum is different, but closely related to those of the isolated membrane bound monomer and the liposome assocd. monomeric and **pentameric** toxin. This leads to the conclusion that contact with detergents or lipids introduce an increase of .beta.-structure. This might expose a hydrophobic surface of the cytotoxin mol. that facilitates oligomerization as well as membrane insertion.

IT Oligomerization
Pseudomonas aeruginosa
Secondary structure (**protein**)
(**oligomerization** and structural changes of Pseudomonas aeruginosa cytotoxin)

L13 ANSWER 46 OF 61 CAPLUS COPYRIGHT 2000 ACS DUPLICATE 9
AN 1996:314952 CAPLUS
DN 125:2858
TI Sex-specific and non-sex-specific oligomerization domains in both of the doublesex transcription factors from Drosophila melanogaster
AU An, Wenqian; Cho, Sayeon; Ishii, Haruhiko; Wensink, Pieter C.
CS Department Biochemistry, Brandeis University, Waltham, MA, 02254-9110, USA
SO Mol. Cell. Biol. (1996), 16(6), 3106-3111
CODEN: MCEBD4; ISSN: 0270-7306
DT Journal
LA English
AB The doublesex gene of Drosophila melanogaster encodes the alternatively spliced, sex-specific transcription factors DSXM and DSXF. These factors regulate male- and female-specific transcription of many genes. For example, female-specific transcription of the yolk protein 1 gene is regulated by DSXM repression in males and DSXF activation in females. In this study we used in vitro interaction assays and the in vivo yeast two-hybrid method to identify and examine oligomerization domains of the DSX proteins. A 66-amino-acid segment common to both **proteins** (amino acids 39 to 104) contains a sequence-specific DNA binding domain and an **oligomerization** domain (OD1). The OD1 domain oligomerizes up to at least a **pentamer**, but only dimers bound to a palindromic regulatory site in the yolk protein 1 gene are detected. Both subunits of the OD1 dimer are in contact with DNA. Another segment of each protein (amino acids 350 to 412 for DSXF and 350 to 427 for DSXM) contains a second oligomerization domain (OD2F and OD2M, resp.). The OD2 domains have both sex-specific and non-sex-specific sequences which are necessary for oligomerization. On the basis of sequence anal., we predict that OD2 oligomerizes through coiled-coil interactions. We speculate that the common function of OD1 and OD2 is to oligomerize the full-length proteins, whereas their specialized functions are to form a dimeric DNA binding unit and a sex-specific transcriptional activation or repression unit.

AB The doublesex gene of Drosophila melanogaster encodes the alternatively spliced, sex-specific transcription factors DSXM and DSXF. These factors regulate male- and female-specific transcription of many genes. For example, female-specific transcription of the yolk protein 1 gene is regulated by DSXM repression in males and DSXF activation in females. In this study we used in vitro interaction assays and the in vivo yeast two-hybrid method to identify and examine oligomerization domains of the DSX proteins. A 66-amino-acid segment common to both **proteins** (amino acids 39 to 104) contains a sequence-specific DNA binding domain and an **oligomerization** domain (OD1). The OD1 domain oligomerizes up to at least a **pentamer**, but only dimers bound to

a palindromic regulatory site in the yolk protein 1 gene are detected. Both subunits of the OD1 dimer are in contact with DNA. Another segment of each protein (amino acids 350 to 412 for DSXF and 350 to 427 for DSXM) contains a second oligomerization domain (OD2F and OD2M, resp.). The OD2 domains have both sex-specific and non-sex-specific sequences which are necessary for oligomerization. On the basis of sequence anal., we predict that OD2 oligomerizes through coiled-coil interactions. We speculate that the common function of OD1 and OD2 is to oligomerize the full-length proteins, whereas their specialized functions are to form a dimeric DNA binding unit and a sex-specific transcriptional activation or repression unit.

L13 ANSWER 47 OF 61 BIOSIS COPYRIGHT 2000 BIOSIS DUPLICATE 10
AN 1996:533580 BIOSIS
DN PREV199699255936
TI The crystal structure of a five-stranded coiled coil in COMP: A prototype ion channel.
AU Malashkevich, Vladimir N. (1); Kammerer, Richard A.; Efimov, Vladimir P.; Schulthess, Therese; Engel, Juergen
CS (1) Dep. Structural Biol., Biozentrum, Univ. Basel, Klingelbergstrasse 70, CH-4056 Basel Switzerland
SO Science (Washington D C), (1996) Vol. 274, No. 5288, pp. 761-765. ISSN: 0036-8075.
DT Article
LA English
AB Oligomerization by the formation of alpha-helical bundles is common in many **proteins**. The crystal structure of a parallel **pentameric** coiled coil, constituting the **oligomerization** domain in the cartilage oligomeric matrix protein (COMP), was determined at 2.05 angstroms resolution. The same structure probably occurs in two other extracelLular matrix proteins, thrombospondins 3 and 4. Complementary hydrophobic interactions and conserved disulfide bridges between the alpha helices result in a thermostable structure with unusual properties. The long hydrophobic axial pore is filled with water molecules but can also accommodate small apolar groups. An "ion trap" is formed inside the pore by a ring of conserved glutamines, which binds chloride and probably other monatomic anions. The oligomerization domain of COMP has marked similarities with proposed models of the **pentameric** transmembrane ion channels in phospholamban and the acetylcholine receptor.
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L13 ANSWER 51 OF 61 CAPLUS COPYRIGHT 2000 ACS
AN 1994:403573 CAPLUS
DN 121:3573
TI Mitochondrial Mas70p signal anchor sequence. Mutations in the transmembrane domain that disrupt dimerization but not targeting or membrane insertion
AU Millar, Douglas G.; Shore, Gordon C.
CS Dep. Biochem., McGill Univ., Montreal, PQ, H3G 1Y6, Can.
SO J. Biol. Chem. (1994), 269(16), 12229-32
CODEN: JBCHA3; ISSN: 0021-9258

DT Journal
LA English
AB Protein Mas70p is an integral membrane protein in Saccharomyces cerevisiae
that is targeted and inserted into the mitochondrial outer membrane in an Nin-Ccyto orientation by its N-terminal 29-amino acid signal anchor sequence. Recently, the authors demonstrated that the signal anchor was capable of mediating homo-oligomerization of a fusion protein, pOMD29, in the outer membrane in vitro. Consistent with this finding, the authors show here that a synthetic peptide corresponding to the Mas70p signal anchor is capable of independent membrane insertion and dimerization with pOMD29. To further map the oligomerization domain in the signal anchor sequence, a deletion mutant of pOMD29 that lacks amino acids 2-10 was constructed. This protein, pOMD29.DELTA.2-10, efficiently participated in
dimer formation following import, indicating that dimerization was mediated by the putative membrane spanning segment (amino acids 11-29). This segment was predicted to form an .alpha.-helix that has an alanine-rich face and contains multiple copies of a **pentapeptide** dimerization motif that is widespread among members of the receptor tyrosine kinase family. Substitution of the alanine residues in one of these copies with isoleucine, producing a potentially bulkier contact surface, resulted in a protein which was targeted and inserted into the outer membrane but failed to assemble into dimers. Taken together, these results identify a structural feature of the signal anchor transmembrane domain that is important for oligomerization but is not required for targeting and membrane insertion.
AB Protein Mas70p is an integral membrane protein in Saccharomyces cerevisiae
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ST mitochondria **protein** Mas70p **oligomerization** domain localization
IT Mitochondria
(**protein** Mas70p of, of Saccharomyces cerevisiae, localization of **oligomerization** region of signal anchor transmembrane domain of)
IT **Proteins**, specific or class
RL: BIOL (Biological study)
(MAS70 (mitochondrial assembly, 70,000-mol.-wt.), of Saccharomyces cerevisiae, localization of **oligomerization** region of signal anchor transmembrane domain of)

L13 ANSWER 52 OF 61 USPATFULL

AN 93:24822 USPATFULL
TI Generation and selection of novel DNA-binding proteins and polypeptides
IN Ladner, Robert C., Ijamsville, MD, United States
Guterman, Sonia K., Belmont, MA, United States
Kent, Rachel B., Boxborough, MA, United States
Ley, Arthur C., Newton, MA, United States
PA Protein Engineering Corp., Cambridge, MA, United States (U.S. corporation)
PI US 5198346 19930330
AI US 1990-558011 19900726 (7)
RLI Continuation-in-part of Ser. No. US 1989-293980, filed on 6 Jan 1989, now patented, Pat. No. US 5096815
DT Utility
EXNAM Primary Examiner: Lacey, David L.; Assistant Examiner: Ulm, John D.
LREP Cooper, Iver P.
CLMN Number of Claims: 48
ECL Exemplary Claim: 24
DRWN 16 Drawing Figure(s); 16 Drawing Page(s)
LN.CNT 10332
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Novel DNA-binding proteins, especially repressors of gene expression, are obtained by variegation of genes encoding known binding proteins and selection for proteins binding the desired target DNA sequence. A novel selection vector may be used to reduce artifacts. Heterooligomeric proteins which bind to a target DNA sequence which need not be palindromic are obtained by a variety of methods, e.g., variegation to obtain proteins binding symmetrized forms of the half-targets and heterodimerization to obtain a protein binding the entire asymmetric target.
DETD . . . of full-length polypeptides. Thus it is preferred that the gene containing the amber, ochre, or opal mutations code for a **protein** that acts as a monomer. Inhibition of **oligomerization** can also be avoided by placing the amber, ochre, or opal mutations very near the amino terminus of the protein. . .
DETD The P22 Mnt repressor, like lambda Cro, is a small **protein** containing both DNA-binding and **oligomerization** sites. Unlike Cro, P22 Mnt is a tetramer in solution (VERS85b, VERS87a). The amino acid sequence of Mnt has been. . .
DETD . . . as the parental DBP, but which prevents oligomerization. It is anticipated that reverse selection will isolate many genes for non-functional **proteins** and that these **proteins** must be analyzed until a suitable **oligomerization**-mutant is found. Therefore, we choose sites carefully so that we maximize the chance of disrupting oligomerization without destroying tertiary structure.. .
DETD It is also possible to modulate DNA-binding specificity by altering the **protein-protein** interface. Because the **oligomerization** equilibrium is coupled to DNA binding, mutations that damage **oligomerization** (see discussion, supra) reduce operator site affinity. Since oligomerization involves the matching of **protein** surfaces, many interactions are hydrophobic in nature and mutations which specifically destabilize **oligomerization** are similar to mutations which destabilize global **protein** structure. Interactions at the site of **oligomerization** can influence the strength of interactions at the DNA-binding site by subtle alterations in protein structure.
DETD GOFF87: Goff, S A, S R Short-Russell, and J F Dice, "Efficient Saturation Mutagenesis of a **Pentapeptide** Coding Sequence Using Mixed Oligonucleotides", DNA (1987), 6(4)381-388.
CLM What is claimed:
. . . the host cell, and (e) forward selecting for expression from a step (c) variegant gene of a second oligomerization mutant **protein**

which is capable of forming a heterooligomer with said first **oligomerization** mutant protein, said heterooligomer binding said ultimate target DNA sequence, and (f) isolating the genes encoding said heterooligomer.

L13 ANSWER 53 OF 61 CAPLUS COPYRIGHT 2000 ACS
AN 1993:535215 CAPLUS
DN 119:135215
TI Membrane orientation and oligomerization of the small hydrophobic protein of human respiratory syncytial virus
AU Collins, Peter L.; Mottet, Genevieve
CS Lab. Infect. Dis., Natl. Inst. Allergy Infect. Dis., Bethesda, MD, 20892, USA
SO J. Gen. Virol. (1993), 74(7), 1445-50
CODEN: JGVIAY; ISSN: 0022-1317
DT Journal
LA English
AB Previous work has demonstrated that the small hydrophobic (SH) protein of human respiratory syncytial virus (RSV) A2 strain is a 64 amino acid integral membrane protein that accumulates intracellularly as an unglycosylated major species (SH0), a minor species truncated at the amino terminus and two N-glycosylated species one of which contains a further addn. of polylactosamine. In this study, the membrane orientation of SH0 was mapped by trypsinization of intact RSV-infected cells followed by washout, lysis and immunopptn. of protected fragments with antisera specific for the protein termini. This showed that the C terminus is extracellular and the SH protein was not detectably palmitylated. Anal. of the SH protein by sedimentation on sucrose gradients showed that it rapidly assembles into a homo-oligomer that co-sediments with the f protein tetramer. Interestingly, all forms of the SH protein were found in the oligomeric fraction. Chem. crosslinking generated species which appeared to represent dimers, trimers, tetramers and **pentamers** as well as a minor species of 180K which might correspond to the oligomeric form detected by sucrose gradient sedimentation.
AB Previous work has demonstrated that the small hydrophobic (SH) protein of human respiratory syncytial virus (RSV) A2 strain is a 64 amino acid integral membrane protein that accumulates intracellularly as an unglycosylated major species (SH0), a minor species truncated at the amino terminus and two N-glycosylated species one of which contains a further addn. of polylactosamine. In this study, the membrane orientation of SH0 was mapped by trypsinization of intact RSV-infected cells followed by washout, lysis and immunopptn. of protected fragments with antisera specific for the protein termini. This showed that the C terminus is extracellular and the SH protein was not detectably palmitylated. Anal. of the SH protein by sedimentation on sucrose gradients showed that it rapidly assembles into a homo-oligomer that co-sediments with the f protein tetramer. Interestingly, all forms of the SH protein were found in the oligomeric fraction. Chem. crosslinking generated species which appeared to represent dimers, trimers, tetramers and **pentamers** as well as a minor species of 180K which might correspond to the oligomeric form detected by sucrose gradient sedimentation.
ST respiratory syncytial virus **protein oligomerization**
IT **Proteins**, specific or class
RL: RCT (Reactant)
(SH (small hydrophobic), of human respiratory syncytial virus, membrane orientation and **oligomerization** of, in infected cells)
IT Animal cell
(disease, infection, with human respiratory syncytial virus, viral small hydrophobic **protein** membrane orientation and **oligomerization** in)
IT Virus, animal

(human respiratory syncytial, small hydrophobic **protein** of, membrane orientation and **oligomerization** of, in infected cells)

L13 ANSWER 57 OF 61 CAPLUS COPYRIGHT 2000 ACS
AN 1992:126527 CAPLUS
DN 116:126527
TI Defined chemically cross-linked oligomers of human C-reactive protein: characterization and reactivity with the complement system
AU Jiang, H.; Lint, T. F.; Gewurz, H.
CS Dep. Immunol./Microbiol., Rush Med. Coll., Chicago, IL, 60612, USA
SO Immunology (1991), 74(4), 725-31
CODEN: IMMUAM; ISSN: 0019-2805
DT Journal
LA English
AB Chem. cross-linked C-reactive protein (CRP) oligomers were prepd. and characterized, and C1q binding and complement (C) activation were investigated. Purified human CRP was polymd. in the presence of both non-cleavable and cleavable crosslinking agents and further sepd. by Superose 12 anal. FPLC column chromatog. into fractions of 110 KDa (**pentameric** monomers), 220 KDa (dimers) and 330 KDa (trimers); virtually no larger oligomers were formed under a variety of exptl. conditions. CRP subunits were cross-linked both within and between CRP **pentamers**. CRP trimers retained native CRP antigenicity without expression of neo-CRP epitopes. CRP trimers showed maximal binding and CRP dimers showed partial binding of solid phase C1q while CRP monomers bound virtually no C1q at all; CRP trimers also bound to fluid phase C1q. Binding was Ca2+ independent and increased as the ionic strength or pH were lowered, characteristics comparable to binding of aggregated IgG to C1q; it was not inhibited by phosphorylcholine. CRP trimers consumed total C, C1 and C2 hemolytic activities upon incubation in fresh human serum, but much less efficiently than did CRP-protamine complexes or aggregated IgG. CRP trimers failed to deplete alternative C pathway hemolytic activity at all. The stable, chem. defined CRP oligomers described in this report, which bind C1q efficiently but display poor ability to activate the classical C pathway in the absence of an appropriate ligand, should be valuable in further studies of the interactions between CRP and the C system.
AB Chem. cross-linked C-reactive protein (CRP) oligomers were prepd. and characterized, and C1q binding and complement (C) activation were investigated. Purified human CRP was polymd. in the presence of both non-cleavable and cleavable crosslinking agents and further sepd. by Superose 12 anal. FPLC column chromatog. into fractions of 110 KDa (**pentameric** monomers), 220 KDa (dimers) and 330 KDa (trimers); virtually no larger oligomers were formed under a variety of exptl. conditions. CRP subunits were cross-linked both within and between CRP **pentamers**. CRP trimers retained native CRP antigenicity without expression of neo-CRP epitopes. CRP trimers showed maximal binding and CRP dimers showed partial binding of solid phase C1q while CRP monomers bound virtually no C1q at all; CRP trimers also bound to fluid phase C1q. Binding was Ca2+ independent and increased as the ionic strength or pH were lowered, characteristics comparable to binding of aggregated IgG to C1q; it was not inhibited by phosphorylcholine. CRP trimers consumed total C, C1 and C2 hemolytic activities upon incubation in fresh human serum, but much less efficiently than did CRP-protamine complexes or aggregated IgG. CRP trimers failed to deplete alternative C pathway hemolytic activity at all. The stable, chem. defined CRP oligomers described in this report, which bind C1q efficiently but display poor ability to activate the classical C pathway in the absence of an appropriate ligand, should be valuable in further studies of the interactions between CRP and the C system.
IT 81069-02-5 82436-77-9
RL: BIOL (Biological study)
(C-reactive **protein oligomerization** by, human classical complement pathway activation in relation to)

L13 ANSWER 59 OF 61 CAPLUS COPYRIGHT 2000 ACS DUPLICATE 14
AN 1988:626424 CAPLUS
DN 109:226424
TI Coordinated assembly of multisubunit **proteins**: **oligomerization** of bacterial enterotoxins in vivo and in vitro
AU Hardy, Simon J. S.; Holmgren, Jan; Johansson, Susanne; Sanchez, Joaquin; Hirst, Timothy R.
CS Dep. Biol., Univ. York, York, YO1 5DD, UK
SO Proc. Natl. Acad. Sci. U. S. A. (1988), 85(19), 7109-13
CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB The assembly, in vivo and in vitro, of a family of hexameric, heat-labile enterotoxins produced by diarrheagenic bacteria was studied. The toxins, which consist of an A subunit and 5 B subunits, are assembled by a highly coordinated process that ensures secretion of the holotoxin complex. It was shown that (1) oxidn. of cysteine residues in the B subunits is a prerequisite step in vivo formation of B-subunit **pentamers**, (2) redn. of dissocd. B subunits in vitro abolishes their ability to reassemble, (3) the kinetics of B-**pentamer** assembly in vivo can be mimicked under defined conditions in vitro, (4) A subunits cannot assoc. with fully assembled B **pentamers** in vitro, and (5) A subunits cause an .apprx.3-fold acceleration in the rate of B-subunit **pentamerization** in vivo, implying that A subunits play a coordinating role in the pathway of holotoxin assembly. The last finding is likely to be of general significance, since it provides a mechanism for preferentially excluding or favoring certain intermediates in the assembly of multisubunit proteins.
TI Coordinated assembly of multisubunit **proteins**: **oligomerization** of bacterial enterotoxins in vivo and in vitro
AB The assembly, in vivo and in vitro, of a family of hexameric, heat-labile enterotoxins produced by diarrheagenic bacteria was studied. The toxins, which consist of an A subunit and 5 B subunits, are assembled by a highly coordinated process that ensures secretion of the holotoxin complex. It was shown that (1) oxidn. of cysteine residues in the B subunits is a prerequisite step in vivo formation of B-subunit **pentamers**, (2) redn. of dissocd. B subunits in vitro abolishes their ability to reassemble, (3) the kinetics of B-**pentamer** assembly in vivo can be mimicked under defined conditions in vitro, (4) A subunits cannot assoc. with fully assembled B **pentamers** in vitro, and (5) A subunits cause an .apprx.3-fold acceleration in the rate of B-subunit **pentamerization** in vivo, implying that A subunits play a coordinating role in the pathway of holotoxin assembly. The last finding is likely to be of general significance, since it provides a mechanism for preferentially excluding or favoring certain intermediates in the assembly of multisubunit proteins.

Chimeric Genes S D + F (P. 13) Amt of soluble (P is lower P13)

Didn't test ~~F~~ - Slavin - Nature, 1978, 272; 624-626 Feeder + bathes with it

because unsolicited cysteine present - get denied p. 13

The acceptor only

PAF-F pentamers p. is a control → doesn't inhibit

1994 - FEBS Letters, 341, 54-58

p. 14

BCL1

all of them come from clones for BCL1

if they have

Nature, 1993, 363: 446-448

S+F - Hinge Region

Thrombospondin 4

Inhibits Anti-ID 9-10 B1 - Against a specific Ab

Third made 3 of them → (S-D-F)

S+F are expressed at high levels

S = 85 KDA

F = 90 + 180